

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Ashkenazi et al.
- (ii) TITLE OF INVENTION: RTD Receptor
- 10 (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Genentech, Inc.
- (B) STREET: 1 DNA Way
- 15 (C) CITY: South San Francisco
- (D) STATE: California
- (E) COUNTRY: USA
- (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
- 20 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WinPatin (Genentech)
- 25 (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- 30 (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Marschang, Diane L.
- (B) REGISTRATION NUMBER: 35,600
- (C) REFERENCE/DOCKET NUMBER: P1129R1
- 35 (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 650/225-5416
- (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 386 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Trp | Gly | Gln | Ser | Val | Pro | Thr | Ala | Ser | Ser | Ala | Arg |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |
| Ala | Gly | Arg | Tyr | Pro | Gly | Ala | Arg | Thr | Ala | Ser | Gly | Thr | Arg | Pro |
| | | | | 20 | | | | | 25 | | | | | 30 |

	Trp	Leu	Leu	Asp	Pro	Lys	Ile	Leu	Lys	Phe	Val	Val	Phe	Ile	Val	
					35					40					45	
5	Ala	Val	Leu	Leu	Pro	Val	Arg	Val	Asp	Ser	Ala	Thr	Ile	Pro	Arg	
					50					55					60	
	Gln	Asp	Glu	Val	Pro	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Gln	Arg	
					65					70					75	
10	Arg	Ser	Leu	Lys	Glu	Glu	Glu	Cys	Pro	Ala	Gly	Ser	His	Arg	Ser	
					80					85					90	
	Glu	Tyr	Thr	Gly	Ala	Cys	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr	
					95					100					105	
15	Thr	Ile	Ala	Ser	Asn	Asn	Leu	Pro	Ser	Cys	Leu	Leu	Cys	Thr	Val	
					110					115					120	
	Cys	Lys	Ser	Gly	Gln	Thr	Asn	Lys	Ser	Ser	Cys	Thr	Thr	Thr	Arg	
20					125					130					135	
	Asp	Thr	Val	Cys	Gln	Cys	Glu	Lys	Gly	Ser	Phe	Gln	Asp	Lys	Asn	
					140					145					150	
25	Ser	Pro	Glu	Met	Cys	Arg	Thr	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	
					155					160					165	
	Met	Val	Lys	Val	Ser	Asn	Cys	Thr	Pro	Arg	Ser	Asp	Ile	Lys	Cys	
					170					175					180	
30	Lys	Asn	Glu	Ser	Ala	Ala	Ser	Ser	Thr	Gly	Lys	Thr	Pro	Ala	Ala	
					185					190					195	
	Glu	Glu	Thr	Val	Thr	Thr	Ile	Leu	Gly	Met	Leu	Ala	Ser	Pro	Tyr	
35					200					205					210	
	His	Tyr	Leu	Ile	Ile	Ile	Val	Val	Leu	Val	Ile	Ile	Leu	Ala	Val	
					215					220					225	
40	Val	Val	Val	Gly	Phe	Ser	Cys	Arg	Lys	Lys	Phe	Ile	Ser	Tyr	Leu	
					230					235					240	
	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Gly	Pro	Glu	Arg	Val	His	
					245					250					255	
45	Arg	Val	Leu	Phe	Arg	Arg	Arg	Ser	Cys	Pro	Ser	Arg	Val	Pro	Gly	
					260					265					270	
	Ala	Glu	Asp	Asn	Ala	Arg	Asn	Glu	Thr	Leu	Ser	Asn	Arg	Tyr	Leu	
50					275					280					285	
	Gln	Pro	Thr	Gln	Val	Ser	Glu	Gln	Glu	Ile	Gln	Gly	Gln	Glu	Leu	

	290	295	300
	Ala Glu Leu Thr Gly Val Thr Val Glu Xaa Pro Glu Glu Pro Gln		
	305	310	315
5	Arg Leu Leu Glu Gln Ala Glu Ala Glu Gly Cys Gln Arg Arg Arg		
	320	325	330
10	Leu Leu Val Pro Val Asn Asp Ala Asp Ser Ala Asp Ile Ser Thr		
	335	340	345
	Leu Leu Asp Ala Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu		
	350	355	360
15	Thr Ile Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu		
	365	370	375
	Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu		
	380	385 386	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

CCAAGTGCAC CTCGGTTCTA TCGATTGAAT TCCCCGGGGA TCCTCTAGAG 50
ATCCCTCGAC CTCGACCCAC GCGTCCGGAA CCTTTGCACG CGCACAAACT 100
ACGGGGACGA TTTCTGATTG ATTTTTGGCG CTTTCGATCC ACCCTCCTCC 150
CTTCTC  ATG GGA CTT TGG GGA CAA AGC GTC CCG ACC GCC 189
      Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala
      1          5          10

TCG AGC GCT CGA GCA GGG CGC TAT CCA GGA GCC AGG ACA 228
Ser Ser Ala Arg Ala Gly Arg Tyr Pro Gly Ala Arg Thr
      15          20

GCG TCG GGA ACC AGA CCA TGG CTC CTG GAC CCC AAG ATC 267
Ala Ser Gly Thr Arg Pro Trp Leu Leu Asp Pro Lys Ile
      25          30          35

CTT AAG TTC GTC GTC TTC ATC GTC GCG GTT CTG CTG CCG 306
Leu Lys Phe Val Val Phe Ile Val Ala Val Leu Leu Pro
      40          45          50

```

		GTC	CGG	GTT	GAC	TCT	GCC	ACC	ATC	CCC	CGG	CAG	GAC	GAA	345
		Val	Arg	Val	Asp	Ser	Ala	Thr	Ile	Pro	Arg	Gln	Asp	Glu	
						55					60				
5		GTT	CCC	CAG	CAG	ACA	GTG	GCC	CCA	CAG	CAA	CAG	AGG	CGC	384
		Val	Pro	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Gln	Arg	Arg	
			65					70					75		
10		AGC	CTC	AAG	GAG	GAG	GAG	TGT	CCA	GCA	GGA	TCT	CAT	AGA	423
		Ser	Leu	Lys	Glu	Glu	Glu	Cys	Pro	Ala	Gly	Ser	His	Arg	
					80					85					
15		TCA	GAA	TAT	ACT	GGA	GCC	TGT	AAC	CCG	TGC	ACA	GAG	GGT	462
		Ser	Glu	Tyr	Thr	Gly	Ala	Cys	Asn	Pro	Cys	Thr	Glu	Gly	
		90					95					100			
		GTG	GAT	TAC	ACC	ATT	GCT	TCC	AAC	AAT	TTG	CCT	TCT	TGC	501
		Val	Asp	Tyr	Thr	Ile	Ala	Ser	Asn	Asn	Leu	Pro	Ser	Cys	
				105					110					115	
20		CTG	CTA	TGT	ACA	GTT	TGT	AAA	TCA	GGT	CAA	ACA	AAT	AAA	540
		Leu	Leu	Cys	Thr	Val	Cys	Lys	Ser	Gly	Gln	Thr	Asn	Lys	
						120					125				
25		AGT	TCC	TGT	ACC	ACG	ACC	AGA	GAC	ACC	GTG	TGT	CAG	TGT	579
		Ser	Ser	Cys	Thr	Thr	Thr	Arg	Asp	Thr	Val	Cys	Gln	Cys	
			130					135					140		
30		GAA	AAA	GGA	AGC	TTC	CAG	GAT	AAA	AAC	TCC	CCT	GAG	ATG	618
		Glu	Lys	Gly	Ser	Phe	Gln	Asp	Lys	Asn	Ser	Pro	Glu	Met	
					145					150					
35		TGC	CGG	ACG	TGT	AGA	ACA	GGG	TGT	CCC	AGA	GGG	ATG	GTC	657
		Cys	Arg	Thr	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val	
		155					160					165			
		AAG	GTC	AGT	AAT	TGT	ACG	CCC	CGG	AGT	GAC	ATC	AAG	TGC	696
		Lys	Val	Ser	Asn	Cys	Thr	Pro	Arg	Ser	Asp	Ile	Lys	Cys	
				170					175					180	
40		AAA	AAT	GAA	TCA	GCT	GCC	AGT	TCC	ACT	GGG	AAA	ACC	CCA	735
		Lys	Asn	Glu	Ser	Ala	Ala	Ser	Ser	Thr	Gly	Lys	Thr	Pro	
						185					190				
45		GCA	GCG	GAG	GAG	ACA	GTG	ACC	ACC	ATC	CTG	GGG	ATG	CTT	774
		Ala	Ala	Glu	Glu	Thr	Val	Thr	Thr	Ile	Leu	Gly	Met	Leu	
			195					200					205		
50		GCC	TCT	CCC	TAT	CAC	TAC	CTT	ATC	ATC	ATA	GTG	GTT	TTA	813
		Ala	Ser	Pro	Tyr	His	Tyr	Leu	Ile	Ile	Ile	Val	Val	Leu	
					210					215					

	GTC	ATC	ATT	TTA	GCT	GTG	GTT	GTG	GTT	GGC	TTT	TCA	TGT	852
	Val	Ile	Ile	Leu	Ala	Val	Val	Val	Val	Gly	Phe	Ser	Cys	
	220					225					230			
5	CGG	AAG	AAA	TTC	ATT	TCT	TAC	CTC	AAA	GGC	ATC	TGC	TCA	891
	Arg	Lys	Lys	Phe	Ile	Ser	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	
			235					240					245	
10	GGT	GGT	GGA	GGA	GGT	CCC	GAA	CGT	GTG	CAC	AGA	GTC	CTT	930
	Gly	Gly	Gly	Gly	Gly	Pro	Glu	Arg	Val	His	Arg	Val	Leu	
					250					255				
15	TTC	CGG	CGG	CGT	TCA	TGT	CCT	TCA	CGA	GTT	CCT	GGG	GCG	969
	Phe	Arg	Arg	Arg	Ser	Cys	Pro	Ser	Arg	Val	Pro	Gly	Ala	
		260					265					270		
	GAG	GAC	AAT	GCC	CGC	AAC	GAG	ACC	CTG	AGT	AAC	AGA	TAC	1008
	Glu	Asp	Asn	Ala	Arg	Asn	Glu	Thr	Leu	Ser	Asn	Arg	Tyr	
				275					280					
20	TTG	CAG	CCC	ACC	CAG	GTC	TCT	GAG	CAG	GAA	ATC	CAA	GGT	1047
	Leu	Gln	Pro	Thr	Gln	Val	Ser	Glu	Gln	Glu	Ile	Gln	Gly	
	285					290					295			
25	CAG	GAG	CTG	GCA	GAG	CTA	ACA	GGT	GTG	ACT	GTA	GAG	TYG	1086
	Gln	Glu	Leu	Ala	Glu	Leu	Thr	Gly	Val	Thr	Val	Glu	Xaa	
			300					305					310	
30	CCA	GAG	GAG	CCA	CAG	CGT	CTG	CTG	GAA	CAG	GCA	GAA	GCT	1125
	Pro	Glu	Glu	Pro	Gln	Arg	Leu	Leu	Glu	Gln	Ala	Glu	Ala	
					315					320				
35	GAA	GGG	TGT	CAG	AGG	AGG	AGG	CTG	CTG	GTT	CCA	GTG	AAT	1164
	Glu	Gly	Cys	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Val	Asn	
		325					330					335		
	GAC	GCT	GAC	TCC	GCT	GAC	ATC	AGC	ACC	TTG	CTG	GAT	GCC	1203
	Asp	Ala	Asp	Ser	Ala	Asp	Ile	Ser	Thr	Leu	Leu	Asp	Ala	
				340					345					
40	TCG	GCA	ACA	CTG	GAA	GAA	GGA	CAT	GCA	AAG	GAA	ACA	ATT	1242
	Ser	Ala	Thr	Leu	Glu	Glu	Gly	His	Ala	Lys	Glu	Thr	Ile	
	350					355					360			
45	CAG	GAC	CAA	CTG	GTG	GGC	TCC	GAA	AAG	CTC	TTT	TAT	GAA	1281
	Gln	Asp	Gln	Leu	Val	Gly	Ser	Glu	Lys	Leu	Phe	Tyr	Glu	
			365					370					375	
50	GAA	GAT	GAG	GCA	GGC	TCT	GCT	ACG	TCC	TGC	CTG	TGAAAG	1320	
	Glu	Asp	Glu	Ala	Gly	Ser	Ala	Thr	Ser	Cys	Leu			
					380					385	386			

AATCTCTTCA GGAAACCAGA GCTTCCCTCA TTTACCTTTT CTCCTACAAA 1370
 GGAAGCAGC CTGGAAGAAA CAGTCCAGTA CTTGACCCAT GGGGCAACAA 1420
 5 ACTCTACTAT CCAATATGGG GCAGCTTACC AATGGTCCTA GAACTTTGTT 1470
 AACGCACTTG GAGTAATTTT TATGAAATAC TGCGTGTGAT AAGCAAACGG 1520
 10 GAGAAATTTA TATCAGATTC TTGGCTGCAT AGTTATACGA TTGTGTATTA 1570
 AGGGTCGTTT TAGGCCACAT GCGGTGGCTC ATGCCTGTAA TCCCAGCACT 1620
 TTGATAGGCT GAGGCAGGTG GATTGCTTGA GCTCGGGAGT TTGAGACCAG 1670
 15 CCTCATCAAC ACAGTGAAAC TCCATCTCAA TTTAAAAAGA AAAAAAGTGG 1720
 TTTTAGGATG TCATTCTTTG CAGTTCTTCA TCATGAGACA AGTCTTTTTT 1770
 TCTGCTTCTT ATATTGCAAG CTCCATCTCT ACTGGTGTGT GCATTTAATG 1820
 20 ACATCTAACT ACAGATGCCG CACAGCCACA ATGCTTTGCC TTATAGTTTT 1870
 TTAACTTTAG AACGGGATTA TCTTGTTATT ACCTGTATTT TCAGTTTCGG 1920
 25 ATATTTTTGA CTTAATGATG AGATTATCAA GACGTACCCC TATGCTAAGT 1970
 CATGAGCATA TGGACTTACG AGGGTTCGAC TTAGAGTTTT GAGCTTTAAG 2020
 ATAGGATTAT TGGGGGCTTA CCCCCACCTT AATTAGAAGA AACATTTTAT 2070
 30 ATTGCTTTAC TA 2082

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATAAAAGTT CCTGCACCAT GACCAGAGAC ACAGTGTGTC AGTGTAAGA 50

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTTCAGGAAA CCAGAGCTTC CCTC 24

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTCTCCCGTT TGCTTATCAC ACGC 24

CTTCAGGAAA CCAGAGCTTC CCTC 24